AMENDMENTS TO THE CLAIMS

Please replace all previous claims with the following listing of claims:

Listing of Claims

1. (Previously presented): Factor RecA comprising an amino acid sequence that is at least 96% identical to the amino acid of SEQ ID NO: 2.

2. (Previously presented): The factor of claim 1 comprising an amino acid sequence that is at least 96.5% identical to the amino acid sequence of SEQ ID NO: 2.

Claims 3–4 (Canceled)

5. (Previously presented): A nucleic acid encoding a factor RecA, wherein the nucleotide sequence is at least 85% identical to the nucleotide sequence of SEQ ID NO: 1.

6. (Previously presented): The nucleic acid of claim 5, wherein the nucleotide sequence is at least 87.5% identical to the nucleotide sequence to the nucleotide sequence of SEQ ID NO: 1.

7. (Previously presented): The nucleic acid of claim 5, encoding for a factor RecA, wherein the amino acid sequence is at least 96% identical to the amino acid sequence of SEQ ID NO: 2.

8. (Previously presented): A method of functionally inactivating the gene *recA* in a gram-positive bacterium that is not *Bacillus megaterium*, said method comprising the step of inactivating said *recA* gene with a nucleic acid sequence that encodes a factor RecA.

9. (Previously presented): The method of claim 8, wherein a nucleic acid that encodes for a non-active protein is introduced with a point mutation.

10. (Previously presented): The method of claim 8, wherein a nucleic acid with a deletion mutation or insertion mutation is employed comprising each of the boundary sequences that comprise at least 70 to 150 nucleic acid positions of the region encoding the protein.

11. (Previously presented): The method of claim 8, wherein nucleic acids with a total of two nucleic acid segments are employed that each comprise at least 70 to 150 nucleic acid positions and thereby at least partially flank the region encoding the protein.

12. (Canceled)

13. (Previously presented): The method of claim 8, wherein the gram-positive bacterium is naturally capable of sporulation and a gene from the phase IV of the sporulation is simultaneously functionally inactivated with *recA*.

14. (Previously presented): The method of claim 13, wherein the inactivated gene from the phase IV sporulation in the nomenclature of *B. subtilis* concerns one of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB* or *yqfD* or homologue thereof.

15. (Canceled)

16. (Previously presented): The method of claim 14, wherein the functional inactivation of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB, yqfD* or *spoIV* or of each of their homologous genes occurs with the help of the sequences SEQ ID NO. 3, 5, 7, 9, 11, 13, 15 or 17 or parts thereof.

17. (Previously presented): A gram-positive bacterium that is not *Bacillus megaterium* in which the gene *recA* is functionally inactivated.

18. (Previously presented): The gram-positive bacterium of claim 17, wherein the functional inactivation is effected through point mutagenesis, partial deletion or insertion or total deletion of the encoding region for the complete protein.

19. (Previously presented): The gram-positive bacterium of claim 17, wherein the functional inactivation is effected through a nucleic acid which comprises a nucleotide sequence at least 85% identical to SEQ ID NO: 1.

20. (Previously presented): The gram-positive bacterium of claim 17, wherein said bacterium is naturally capable of sporulation and by which a gene from phase IV of the sporulation is simultaneously functionally inactivated with *recA*.

21. (Previously presented): The gram-positive bacterium of claim 20, wherein the inactivated gene from the phase IV of the sporulation in the nomenclature of *B. subtilis* concerns one of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB* or *yqfD* or homologue thereof.

22. (Canceled)

23. (Previously presented): The gram-positive bacterium of claim 21, wherein the functional inactivation of the genes *spoIVA, spoIVB, spoIVCA, spoIVCB, spoIVFA, spoIVFB, yqfD* or *spoIV* or of each of their homologous genes is effected with the help of the sequences SEQ ID NO. 3, 5, 7, 9, 11, 13, 15 or 17 or parts thereof.

24. (Previously presented): The gram-positive bacterium of claim 17, wherein said bacterium is from the genus *Clostridium* or *Bacillus*.

25. (Previously presented): A process for fermenting a gram-positive bacterium comprising the step of fermenting the gram-positive bacterium of claim 17.

26. (Previously presented): The process of claim 25, wherein said gram-positive bacterium produces a low molecular weight compound or a protein.

27. (Previously presented): The process of claim 26, wherein the low molecular weight compound is a natural product, a nutritional supplement or a pharmaceutically relevant compound.

28. (Previously presented): The process of claim 26, wherein the protein is an enzyme.

29. (Previously presented): A method for improving a molecular biological reaction comprising adding the factor RecA of claim 1.

30. (Previously presented): The method of claim 29, wherein the molecular biological reaction comprises stabilizing single stranded DNA in a DNA polymerization, recombination processes *in vitro*, or converting double stranded DNA into single stranded DNA or vice versa.

31. (Previously presented): A vector comprising the nucleic acid of claim 5.

32. (Previously presented): The vector of claim 31, wherein said vector is an expression vector.

33. (Previously presented): A process for the manufacture of the factor RecA of claim 1.

34. (Currently amended): The process of claim 33, comprising adding ~~the nucleic acid of claim 1~~ to a host cell a nucleic acid encoding a factor RecA, wherein the nucleotide sequence is at least 85% identical to the nucleotide sequence of SEQ ID NO: 1.

Claims 35–47 (Canceled)

48. (Previously presented) The method of claim 8, wherein said nucleic acid sequence comprises a nucleotide sequence at least 85% identical to SEQ ID NO: 1.

49. (Previously presented): A method for inactivating a factor *rec*A gene *in vitro* comprising interaction of the nucleic acid of claim 5 with an associated nucleic acid.

50. (Previously presented): A method for amplifying a DNA region *in vivo* comprising orienting against one another two nucleic acids selected from the group consisting of nucleic acids having the sequences of SEQ ID NOs: 25 to 30.

51. (Previously presented): The method claim 50, wherein the DNA region is a *recA* gene.

52. (Previously presented): The method of claim 50, wherein the DNA region is a *spoIV* gene.

53. (Previously presented): The method of claim 52, further comprising a gram-positive bacterium that is naturally capable of sporulation that is not *Bacillus megaterium*, and wherein a gene from phase IV of sporulation is simultaneously functionally inactivated with *recA*.

54. (Currently amended): A method for producing the gram-positive bacterium of claim 20 comprising ~~the method of claim 52~~ amplifying a *spoIV* DNA region *in vivo* comprising orienting against one another two nucleic acids selected from the group consisting of nucleic acids having the sequences of SEQ ID NOs: 25 to 30.